

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/562,132
Source: IFWP
Date Processed by STIC: 3/6/07

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 03/06/2007

PATENT APPLICATION: US/10/562,132

TIME: 08:51:32

Input Set : A:\126446.ST25.txt

Output Set: N:\CRF4\03062007\J562132.raw

3 <110> APPLICANT: Pedersen, Susanne
 4 Cole, Robert
 5 Wienberger, Ron
 6 Sloane, Andrew
 8 <120> TITLE OF INVENTION: Method of isolating a protein
 10 <130> FILE REFERENCE: FBR0005-100
 12 <140> CURRENT APPLICATION NUMBER: 10/562,132
 C--> 14 <141> CURRENT FILING DATE: 2005-12-23
 14 <150> PRIOR APPLICATION NUMBER: AU 2003903317
 15 <151> PRIOR FILING DATE: 2003-06-27
 17 <150> PRIOR APPLICATION NUMBER: PCT/AU2004/00856
 18 <151> PRIOR FILING DATE: 2004-06-28
 20 <160> NUMBER OF SEQ ID NOS: 26
 22 <170> SOFTWARE: PatentIn version 3.3
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 593
 26 <212> TYPE: PRT
 27 <213> ORGANISM: Streptococcus sp.
 29 <400> SEQUENCE: 1
 31 Met Glu Lys Glu Lys Lys Val Lys Tyr Phe Leu Arg Lys Ser Ala Phe
 32 1 5 10 15
 35 Gly Leu Ala Ser Val Ser Ala Ala Phe Leu Val Gly Ser Thr Val Phe
 36 20 25 30
 39 Ala Val Asp Ser Pro Ile Glu Asp Thr Pro Ile Ile Arg Asn Gly Gly
 40 35 40 45
 43 Glu Leu Thr Asn Leu Leu Gly Asn Ser Glu Thr Thr Leu Ala Leu Arg
 44 50 55 60
 47 Asn Glu Glu Ser Ala Thr Ala Asp Leu Thr Ala Ala Ala Val Ala Asp
 48 65 70 75 80
 51 Thr Val Ala Ala Ala Ala Ala Glu Asn Ala Gly Ala Ala Ala Trp Glu
 52 85 90 95
 55 Ala Ala Ala Ala Ala Asp Ala Leu Ala Lys Ala Lys Ala Asp Ala Leu
 56 100 105 110
 59 Lys Glu Phe Asn Lys Tyr Gly Val Ser Asp Tyr Tyr Lys Asn Leu Ile
 60 115 120 125
 63 Asn Asn Ala Lys Thr Val Glu Gly Val Lys Asp Leu Gln Ala Gln Val
 64 130 135 140
 67 Val Glu Ser Ala Lys Lys Ala Arg Ile Ser Glu Ala Thr Asp Gly Leu
 68 145 150 155 160
 71 Ser Asp Phe Leu Lys Ser Gln Thr Pro Ala Glu Asp Thr Val Lys Ser
 72 165 170 175
 75 Ile Glu Leu Ala Glu Ala Lys Val Leu Ala Asn Arg Glu Leu Asp Lys
 76 180 185 190

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79 Tyr Gly Val Ser Asp Tyr His Lys Asn Leu Ile Asn Asn Ala Lys Thr
80      195                200                205
83 Val Glu Gly Val Lys Asp Leu Gln Ala Gln Val Val Glu Ser Ala Lys
84      210                215                220
87 Lys Ala Arg Ile Ser Glu Ala Thr Asp Gly Leu Ser Asp Phe Leu Lys
88 225                230                235                240
91 Ser Gln Thr Pro Ala Glu Asp Thr Val Lys Ser Ile Glu Leu Ala Glu
92      245                250                255
95 Ala Lys Val Leu Ala Asn Arg Glu Leu Asp Lys Tyr Gly Val Ser Asp
96      260                265                270
99 Tyr Tyr Lys Asn Leu Ile Asn Asn Ala Lys Thr Val Glu Gly Val Lys
100     275                280                285
103 Ala Leu Ile Asp Glu Ile Leu Ala Ala Leu Pro Lys Thr Asp Thr Tyr
104     290                295                300
107 Lys Leu Ile Leu Asn Gly Lys Thr Leu Lys Gly Glu Thr Thr Thr Glu
108 305                310                315                320
111 Ala Val Asp Ala Ala Thr Ala Glu Lys Val Phe Lys Gln Tyr Ala Asn
112     325                330                335
115 Asp Asn Gly Val Asp Gly Glu Trp Thr Tyr Asp Asp Ala Thr Lys Thr
116     340                345                350
119 Phe Thr Val Thr Glu Lys Pro Glu Val Ile Asp Ala Ser Glu Leu Thr
120     355                360                365
123 Pro Ala Val Thr Thr Tyr Lys Leu Val Ile Asn Gly Lys Thr Leu Lys
124     370                375                380
127 Gly Glu Thr Thr Thr Glu Ala Val Asp Ala Ala Thr Ala Glu Lys Val
128 385                390                395                400
131 Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu Trp Thr Tyr
132     405                410                415
135 Asp Asp Ala Thr Lys Thr Phe Thr Val Thr Glu Lys Pro Glu Val Ile
136     420                425                430
139 Asp Ala Ser Glu Leu Thr Pro Ala Val Thr Thr Tyr Lys Leu Val Ile
140     435                440                445
143 Asn Gly Lys Thr Leu Lys Gly Glu Thr Thr Thr Lys Ala Val Asp Ala
144     450                455                460
147 Glu Thr Ala Glu Lys Ala Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val
148 465                470                475                480
151 Asp Gly Val Trp Thr Tyr Asp Asp Ala Thr Lys Thr Phe Thr Val Thr
152     485                490                495
155 Glu Met Val Thr Glu Val Pro Gly Asp Ala Pro Thr Glu Pro Glu Lys
156     500                505                510
159 Pro Glu Ala Ser Ile Pro Leu Val Pro Leu Thr Pro Ala Thr Pro Ile
160     515                520                525
163 Ala Lys Asp Asp Ala Lys Lys Asp Asp Thr Lys Lys Glu Asp Ala Lys
164     530                535                540
167 Lys Pro Glu Ala Lys Lys Glu Asp Ala Lys Lys Ala Glu Thr Leu Pro
168 545                550                555                560
171 Thr Thr Gly Glu Gly Ser Asn Pro Phe Phe Thr Ala Ala Ala Leu Ala
172     565                570                575
175 Val Met Ala Gly Ala Gly Ala Leu Ala Val Ala Ser Lys Arg Lys Glu

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176          580          585          590
179 Asp
183 <210> SEQ ID NO: 2
184 <211> LENGTH: 454
185 <212> TYPE: PRT
186 <213> ORGANISM: Staphylococcus aureus
188 <400> SEQUENCE: 2
190 Met Met Thr Leu Gln Ile His Thr Gly Gly Ile Asn Leu Lys Lys Lys
191 1          5          10          15
194 Asn Ile Tyr Ser Ile Arg Lys Leu Gly Val Gly Ile Ala Ser Val Thr
195          20          25          30
198 Leu Gly Thr Leu Leu Ile Ser Gly Val Thr Pro Ala Ala Asn Ala
199          35          40          45
202 Ala Gln His Asp Glu Ala Gln Asn Ala Phe Tyr Gln Val Leu Asn
203          50          55          60
206 Met Pro Asn Leu Asn Ala Asp Gln Arg Asn Gly Phe Ile Gln Ser Leu
207 65          70          75          80
210 Lys Asp Asp Pro Ser Gln Ser Ala Asn Val Leu Gly Glu Ala Gln Lys
211          85          90          95
214 Leu Asn Asp Ser Gln Ala Pro Lys Ala Asp Ala Gln Gln Asn Lys Phe
215          100         105         110
218 Asn Lys Asp Gln Gln Ser Ala Phe Tyr Glu Ile Leu Asn Met Pro Asn
219          115         120         125
222 Leu Asn Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp
223          130         135         140
226 Pro Ser Gln Ser Thr Asn Val Leu Gly Glu Ala Lys Lys Leu Asn Glu
227 145         150         155         160
230 Ser Gln Ala Pro Lys Ala Asp Asn Asn Phe Asn Lys Glu Gln Gln Asn
231          165         170         175
234 Ala Phe Tyr Glu Ile Leu Asn Met Pro Asn Leu Asn Glu Glu Gln Arg
235          180         185         190
238 Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn
239          195         200         205
242 Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala
243          210         215         220
246 Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu
247 225         230         235         240
250 His Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser
251          245         250         255
254 Leu Lys Asp Asp Pro Ser Val Ser Lys Glu Ile Leu Ala Glu Ala Lys
255          260         265         270
258 Lys Leu Asn Asp Ala Gln Ala Pro Lys Glu Glu Asp Asn Asn Lys Pro
259          275         280         285
262 Gly Lys Glu Asp Asn Asn Lys Pro Gly Lys Glu Asp Gly Asn Lys Pro
263          290         295         300
266 Gly Lys Glu Asp Asn Lys Lys Pro Gly Lys Glu Asp Gly Asn Lys Pro
267 305         310         315         320
270 Gly Lys Glu Asp Asn Lys Lys Pro Gly Lys Glu Asp Gly Asn Lys Pro
271          325         330         335

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```

274 Gly Lys Glu Asp Gly Asn Lys Pro Gly Lys Glu Asp Gly Asn Lys Pro
275           340           345           350
278 Gly Lys Glu Asp Gly Asn Gly Val His Val Val Lys Pro Gly Asp Thr
279           355           360           365
282 Val Asn Asp Ile Ala Lys Ala Asn Gly Thr Thr Ala Asp Lys Ile Ala
283           370           375           380
286 Val Asp Asn Lys Leu Ala Asp Lys Asn Met Ile Lys Pro Gly Gln Glu
287 385           390           395           400
290 Leu Val Val Asp Lys Lys Gln Pro Ala Asn His Ala Asp Ala Asn Lys
291           405           410           415
294 Ala Gln Ala Leu Pro Glu Thr Gly Glu Glu Asn Pro Phe Ile Gly Thr
295           420           425           430
298 Thr Val Phe Gly Gly Leu Ser Leu Ala Leu Gly Ala Ala Leu Leu Ala
299           435           440           445
302 Gly Arg Arg Arg Glu Leu
303           450
306 <210> SEQ ID NO: 3
307 <211> LENGTH: 719
308 <212> TYPE: PRT
309 <213> ORGANISM: Peptostreptococcus magnus
311 <400> SEQUENCE: 3
313 Met Ala Ala Leu Ala Gly Ala Ile Val Val Thr Gly Gly Val Gly Ser
314 1           5           10           15
317 Tyr Ala Ala Asp Glu Pro Ile Asp Leu Glu Lys Leu Glu Glu Lys Arg
318           20           25           30
321 Asp Lys Glu Asn Val Gly Asn Leu Pro Lys Phe Asp Asn Glu Val Lys
322           35           40           45
325 Asp Gly Ser Glu Asn Pro Met Ala Lys Tyr Pro Asp Phe Asp Asp Glu
326 50           55           60
329 Ala Ser Thr Arg Phe Glu Thr Glu Asn Asn Glu Phe Glu Glu Lys Lys
330 65           70           75           80
333 Val Val Ser Asp Asn Phe Phe Asp Gln Ser Glu His Pro Phe Val Glu
334           85           90           95
337 Asn Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser Glu Glu Glu
338           100          105          110
341 Val Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser Thr Gln Thr
342           115          120          125
345 Ala Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu Ala Tyr Ala
346           130          135          140
349 Tyr Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val
350 145          150          155          160
353 Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys
354           165          170          175
357 Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile
358           180          185          190
361 Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu
362           195          200          205
365 Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu Lys Lys Asp
366           210          215          220

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```

369 Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn
370 225                230                235                240
373 Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu
374                245                250                255
377 Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr
378                260                265                270
381 Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg
382                275                280                285
385 Tyr Ala Asp Leu Leu Ala Lys Glu Asn Gly Lys Tyr Thr Val Asp Val
386                290                295                300
389 Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys
390 305                310                315                320
393 Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile
394                325                330                335
397 Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Ala
398                340                345                350
401 Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Glu
402                355                360                365
405 Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr Thr Ile Asn
406                370                375                380
409 Ile Arg Phe Ala Gly Lys Lys Val Asp Glu Lys Pro Glu Glu Lys Glu
410 385                390                395                400
413 Gln Val Thr Ile Lys Glu Asn Ile Tyr Phe Glu Asp Gly Thr Val Gln
414                405                410                415
417 Thr Ala Thr Phe Lys Gly Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr
418                420                425                430
421 Arg Tyr Ala Asp Leu Leu Ser Lys Glu His Gly Lys Tyr Thr Ala Asp
422                435                440                445
425 Leu Glu Asp Gly Gly Tyr Thr Ile Asn Ile Arg Phe Ala Gly Lys Glu
426                450                455                460
429 Glu Pro Glu Glu Thr Pro Glu Lys Pro Glu Val Gln Asp Gly Tyr Ala
430 465                470                475                480
433 Ser Tyr Glu Glu Ala Glu Ala Ala Ala Lys Glu Ala Leu Lys Asn Asp
434                485                490                495
437 Asp Val Asn Lys Ser Tyr Thr Ile Arg Gln Gly Ala Asp Gly Arg Tyr
438                500                505                510
441 Tyr Tyr Val Leu Ser Pro Val Glu Ala Glu Glu Glu Lys Pro Glu Ala
442                515                520                525
445 Gln Asn Gly Tyr Ala Thr Tyr Glu Glu Ala Glu Ala Ala Lys Lys
446                530                535                540
449 Ala Leu Glu Asn Asp Pro Ile Asn Lys Ser Tyr Ser Ile Arg Gln Gly
450 545                550                555                560
453 Ala Asp Gly Arg Tyr Tyr Val Leu Ser Pro Val Glu Ala Glu Thr
454                565                570                575
457 Pro Glu Lys Pro Val Glu Pro Ser Glu Pro Ser Thr Pro Asp Val Pro
458                580                585                590
461 Ser Asn Pro Ser Asn Pro Ser Thr Pro Asp Val Pro Ser Thr Pro Asp
462                595                600                605
465 Val Pro Ser Asn Pro Ser Thr Pro Glu Val Pro Ser Asn Pro Ser Thr

```

RAW SEQUENCE LISTING ERROR SUMMARY

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5

VERIFICATION SUMMARY

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DATE: 03/06/2007

TIME: 08:51:33

Input Set : A:\126446.ST25.txt

Output Set: N:\CRF4\03062007\J562132.raw

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date